RAW SEQUENCE LISTING
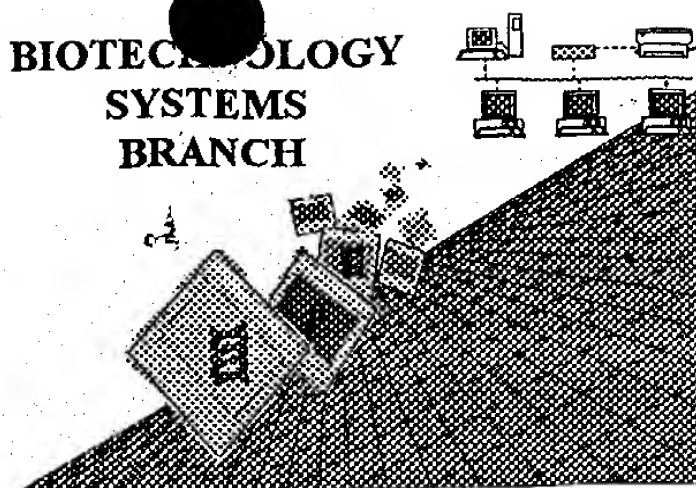# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/807,248*

Source: *OIPE*

Date Processed by STIC: *7/19/2001*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/807248_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                           prevent "wrapping."

2 _____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use space characters, instead.

4 _____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                           ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                           each n or Xaa can only represent a single residue. Please present the maximum number of each
                           residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                           previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                           the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                           Artificial or Unknown sequences.

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                           (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                           (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                           This sequence is intentionally skipped

                           Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES)   <210> sequence id number
                           <400> sequence id number
                           000

9 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                           In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                           is Artificial Sequence

11 _____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                           Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                           "Unknown." Please explain source of genetic material in <220> to <223> section.
                           (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                           listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING   DATE: 07/19/2001
PATENT APPLICATION: US/09/807,248   TIME: 12:23:45

Input Set : A:\BB1208pct seq lst.txt
Output Set: N:\CRF3\07192001\I807248.raw

```
      3 <110> APPLICANT: E. I. du Pont de Nemours and Company
      5 <120> TITLE OF INVENTION: SCORPION TOXINS
      7 <130> FILE REFERENCE: BB1208
C-->  9 <140> CURRENT APPLICATION NUMBER: US/09/807,248
C--> 10 <141> CURRENT FILING DATE: 2001-06-27
     12 <150> PRIOR APPLICATION NUMBER: 60/105,404
     13 <151> PRIOR FILING DATE: 1998-10-23
     15 <160> NUMBER OF SEQ ID NOS: 17
     17 <170> SOFTWARE: Microsoft Office 97
```

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ERRORED SEQUENCES

```
     55 <210> SEQ ID NO: 3
     56 <211> LENGTH: 238
     57 <212> TYPE: DNA
     58 <213> ORGANISM: Leiurus quinquestriatus
     60 <400> SEQUENCE: 3
```
see item 9 on Errn Summary Sheet
```
E--> 61 tagtttggca cttctcttca tgacaggtgt ggagagtgta cgtgacggtt atattgccaa   60
     62 gcccgaaaac tgtgcacacc attgctttcc agggtcctcc ggttgcgaca cattatgtaa  120
     63 ggaaaacggt ggtacgggtg gccattgcgg atttaaagtt ggacatggaa ctgcctgctg  180
     64 gtgcaatgcc ttgcccgata aagtagggat tatagtagat ggagtaaaat gccatcgc    238
    155 <210> SEQ ID NO: 8
    156 <211> LENGTH: 252
    157 <212> TYPE: DNA
    158 <213> ORGANISM: Leiurus quinquestriatus
    160 <400> SEQUENCE: 8
```
see item 9
```
E--> 161 atgaattatt tggtatgat tagtttggca cttctcctca tgacaggtgt ggagagtgga   60
    162 cgtgatgctt atattgccca gaactataac tgtgtatatc attgtgcttt aaatccatat  120
    163 tgcaacgatt tatgtaccaa gaacggtgct aagagtggct attgccaatg gttcggttca  180
    164 agtggaaacg cctgctggtg catagatttg cccgataacg taccgattaa agtaccagga  240
    165 aaatgccatc gc                                                      252
```

see next page

<210> 9
<211> 84
<212> PRT
<213> Leiurus quinquestriatus

<220>
<221> SIGNAL
<222> (1)..(19)

<400> 9

Item 9

```
Met Asn Tyr Leu Val Xaa Ile Ser Leu Ala Leu Leu Leu Met Thr Gly
 1               5                  10                  15

Val Glu Ser Gly Arg Asp Ala Tyr Ile Ala Gln Asn Tyr Asn Cys Val
            20                  25                  30

Tyr His Cys Ala Leu Asn Pro Tyr Cys Asn Asp Leu Cys Thr Lys Asn
        35                  40                  45

Gly Ala Lys Ser Gly Tyr Cys Gln Trp Phe Gly Ser Ser Gly Asn Ala
    50                  55                  60

Cys Trp Cys Ile Asp Leu Pro Asp Asn Val Pro Ile Lys Val Pro Gly
65                  70                  75                  80

Lys Cys His Arg
```

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:61 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:161 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:177 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9